

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/565,418
Source: IFWP
Date Processed by STIC: 1-30-06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 01/30/2006

PATENT APPLICATION: US/10/565,418

TIME: 15:54:11

Input Set : A:\ITR0065YP SEQLIST.TXT

Output Set: N:\CRF4\01302006\J565418.raw

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4 <110> APPLICANT: Monaci, Paolo
5       Gallo, Pasquale
6       Nuzzo, Maurizio
8 <120> TITLE OF INVENTION: SYNTHETIC GENE ENCODING HUMAN EPIDERMAL
9       GROWTH FACTOR 2/NEU ANTIGEN AND USES THEREOF
12 <130> FILE REFERENCE: ITR0065YP
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/565,418
C--> 14 <141> CURRENT FILING DATE: 2006-01-23
14 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/008234
15 <151> PRIOR FILING DATE: 2004-04-20
17 <150> PRIOR APPLICATION NUMBER: 60/489,237
18 <151> PRIOR FILING DATE: 2003-07-21
20 <160> NUMBER OF SEQ ID NOS: 14
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3768
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: HER2opt
32 <400> SEQUENCE: 1
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34 gccagcacc aggtgtgcac cggcaccgac atgaagctgc gcctgcccgc cagccccgag 120
35 acccacctgg acatgctgcg ccacctgtac cagggctgcc aggtggtgca gggcaacctg 180
36 gagctgacct acctgcccac caacgccagc ctgagcttcc tgcaggacat ccaggaggtg 240
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42 ctgaccctga tcgacaccaa ccgcagccgc gcctgccacc cctgcagccc catgtgcaag 600
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48 tacaactacc tgagcaccga cgtgggcagc tgcaccctgg tgtgccccct gcacaaccag 960
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51 atccaggagt tcgcccgtcg caagaagatc ttccggcagc tggccttcct gcccgagagc 1140
52 ttcgacggcg accccggccg caacaccgcc cccctgcagc ccgagcagct gcaggtgttc 1200
53 gagaccctgg aggagatcac cggctacctg tacatcagcg cctggcccga cagcctgccc 1260
54 gacctgagcg tgttcagaa cctgcaggtg atccggcgcc gcactctgca caacggcgcc 1320

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55 tacagcctga ccctgcaggg cctgggcac cagctggctgg gcctgcgcag cctgcgcgag 1380
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57 ccctgggacc agctgttccg caacccccac caggccctgc tgcacaccgc caaccgcccc 1500
58 gaggacgagt gcgtgggcca gggcctggcc tggcaccagc tgtgcgccc cggccactgc 1560
59 tggggccccc gccccacca gtgcgtgaac tgcagccagt tcctgcgcgg ccaggagtgc 1620
60 gtggaggagt gccgcgtgct gcagggcctg cccgcgcagt acgtgaacgc ccgccactgc 1680
61 ctgccctgcc accccgagtg ccagccccag aacggcagcg tgacctgctt cggccccgag 1740
62 gccgaccagt gcgtggcctg cggccactac aaggaccccc ctttctgcgt ggcccgtgc 1800
63 cccagcggcg tgaagcccca cctgagctac atgcccctct ggaagtcccc cgacgaggag 1860
64 ggcgcctgcc agccctgccc catcaactgc acccacagct gcgtggacct ggacgacaag 1920
65 ggctgccccg ccgagcagcg cggcagcccc ctgaccagca tcatcagcgc cgtggtgggc 1980
66 atcctgctgg tgggtggtgct gggcgtgggt ttcggcatcc tgatcaagcg ccgccagcag 2040
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93 ggcggagctg ctctcagcc tcacctcca cctgctttca gccctgcttt cgacaacctg 3660
94 tactactggg accaggaccc tcctgagagg ggtgctctc ctagcacctt caagggcacc 3720
95 cccaccgccc agaacccca gtacctgggc ctggacgtgc ccgtgtaa 3768

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97 <210> SEQ ID NO: 2

98 <211> LENGTH: 1255

99 <212> TYPE: PRT

100 <213> ORGANISM: Homo Sapiens, HER2

102 <400> SEQUENCE: 2

103 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu

104 1 5 10 15

105 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys

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106          20          25          30
107 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
108          35          40          45
109 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
110          50          55          60
111 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
112 65          70          75          80
113 Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
114          85          90          95
115 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
116          100         105         110
117 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
118          115         120         125
119 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
120          130         135         140
121 Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
122 145          150         155         160
123 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
124          165         170         175
125 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
126          180         185         190
127 His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
128          195         200         205
129 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
130          210         215         220
131 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
132 225          230         235         240
133 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
134          245         250         255
135 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
136          260         265         270
137 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
138          275         280         285
139 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
140          290         295         300
141 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
142 305          310         315         320
143 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
144          325         330         335
145 Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
146          340         345         350
147 Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
148          355         360         365
149 Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
150          370         375         380
151 Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
152 385          390         395         400
153 Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
154          405         410         415

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155 Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
156          420          425          430
157 Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
158          435          440          445
159 Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
160          450          455          460
161 Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
162 465          470          475          480
163 Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
164          485          490          495
165 Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
166          500          505          510
167 Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
168          515          520          525
169 Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
170          530          535          540
171 Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
172 545          550          555          560
173 Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
174          565          570          575
175 Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
176          580          585          590
177 Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
178          595          600          605
179 Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
180          610          615          620
181 Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
182 625          630          635          640
183 Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
184          645          650          655
185 Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
186          660          665          670
187 Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
188          675          680          685
189 Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
190          690          695          700
191 Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
192 705          710          715          720
193 Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
194          725          730          735
195 Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
196          740          745          750
197 Ala Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
198          755          760          765
199 Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
200          770          775          780
201 Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
202 785          790          795          800
203 Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg

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204          805          810          815
205 Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
206          820          825          830
207 Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
208          835          840          845
209 Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
210          850          855          860
211 Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
212 865          870          875          880
213 Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
214          885          890          895
215 Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
216          900          905          910
217 Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
218          915          920          925
219 Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
220          930          935          940
221 Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
222 945          950          955          960
223 Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
224          965          970          975
225 Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
226          980          985          990
227 Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
228          995          1000          1005
229 Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu
230          1010          1015          1020
231 Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly
232 1025          1030          1035          1040
233 Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly
234          1045          1050          1055
235 Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg
236          1060          1065          1070
237 Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly
238          1075          1080          1085
239 Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His
240          1090          1095          1100
241 Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu
242 1105          1110          1115          1120
243 Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln
244          1125          1130          1135
245 Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
246          1140          1145          1150
247 Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
248          1155          1160          1165
249 Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
250          1170          1175          1180
251 Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
252 1185          1190          1195          1200

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VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date